Appl. No. 09/917,376 Amdr. Dated: August 20, 2007 Reply to Office action of May 18, 2007

## IN THE SPECIFICATION

Please replace Table 2 with the following replacement Table:

Table 2. Gene/polypeptide segments with amino acid sequences.

SEQ ID NO. (amino acid)	SEQ ID NO. (nucleotide)	AviIII Segment	Segment Data
1	2	Total length	SEQ ID NO: 1 (see Table <u>3</u> [[1]]); SEQ ID NO: 2 (see Table <u>4</u> [[2]])
		Signal (potential)	$\overline{ ext{M}}$ RSRRLVSLLAATASFAVAAALGVL $\overline{ ext{PI}}$ AITASPAH $\overline{ ext{A}}$
		CD (GH74)	ATTQPYTWSNVAIGGGGFVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWPLLD WVGWNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATW QITPLPFKLGGNMPGRGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTDTTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAPTGFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYFGYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDISAEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQIHIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSVDYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGTSVDYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGTVAASADGSRFVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGVTFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAITGVSSAVNVGFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGNWGQAITGDHANLRRVYIGTNGRGIYYGDIGGAPSG
		CBD_III (partial)	<u>V</u> SGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTVRYWFTRDGGSSTLV YNCDWAAIGCGNIRASFGSVNPATPTADTYLQX*
		CBD_III (partial)	<u>V</u> SGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTVRYWFTRDGGSSTLV YNCDWAAIGCGNIRASFGSVNPATPTADTYLQ

Please replace Table 5 with the following replacement Table:

## Table 5. Multiple amino acid sequence alignment of a AviIII catalytic domain and polypeptides with Glycoside Hydrolase Family 74 catalytic domains.

Multialignment of related Glycoside Hydrolase Family 74 catalytic domain GH74\_Ace: Acidothermus cellulolyticus AviIII catalytic domain GH74\_SEQ ID NO: 3

AviIII\_Aac: Aspergillus aculeatus Avicelase III (endoglucanase). GeneBank Acc. # BAA29031 SEQ ID NO: 7

GH74 Ace	ATTOPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
GH74_Ace AviIII_Aac	WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG :.* :::::::::::::::::::::::::::::::::::
GH74_Ace AviIII_Aac	GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS
GH74_Ace AviIII_Aac	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T TYTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY * * * * * * * * * * * * * * * * * * *
GH74_Ace AviIII_Aac	GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISPTSLASTYY
GH74_Ace AviIII_Aac	GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
GH74_Ace AviIII_Aac	AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI NAPWIQDTTSTDQFPVRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV **:: ::*** **:****** :: :: :: :: :: :: :: :
GH74_Ace AviIII_Aac	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI : .:. *:** ** .**:**.* .**:** *** *:*: *: *:
GH74_Ace AviIII_Aac	DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR DYAGNKPSNIVRSGASDDYPTLALSSNFGSTWYADYAASTSTGTGAVALSADGDT *** :** ***:* :*:::: **: * ::* ****.
GH74_Ace AviIII_Aac	FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV VLLMSSTSGALVSKSQGTLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT .:* : : : : : : : : : : : : : : : :
GH74_Ace AviIII_Aac	TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF : : * * * : *
GH74_Ace AviIII_Aac	GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
GH74_ACe AviIII_Aac	LRRVYIGTNGRGIVYGDIGGAPSG YGRVFRGHERPGHLLRQSQREPAG **: *: *: *:*